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166883

From: Whiteman, Brian
Sent: Tuesday, September 27, 2005 8:01 AM
To: STIC-Biotech/ChemLib
Subject: seq search

09/578,453

SEQ ID NO: 1 and 2
1) issued and published US application databases

Thank you,

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Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

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Searcher: _____
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Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 15P
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 05:40:32 ; Search time 94.7368 Seconds
(without alignments)
310.893 Million cell updates/sec

Title: US-09-578-453-1
Perfect score: 18
Sequence: 1 CGACTGTGAATCTCCAT 18
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18	100.0	1415	3	US-09-414-436-2
C 2	16.4	91.1	1173	2	US-08-184-009-214
C 3	16.4	91.1	1173	2	US-08-458-356-214
C 4	16.4	91.1	1173	3	US-08-796-101-45
C 5	16.4	91.1	1173	3	US-08-460-736-214
C 6	16.4	91.1	1173	4	US-09-535-370-214
C 7	16.4	91.1	1173	4	US-09-663-667-214
C 8	15.4	85.6	396	4	US-08-585-593A-36
C 9	15.4	85.6	527	4	US-09-621-976-1600
C 10	15.4	85.6	2516	4	US-09-270-767-14686
C 11	15.4	85.6	103750	4	US-09-949-016-13319
C 12	15	83.3	1024	4	US-09-328-4750-5
C 13	14.8	82.2	1107	4	US-09-248-796A-8906
C 14	14.4	80.0	478	4	US-09-621-976-18989
C 15	14.4	80.0	601	4	US-09-949-016-60603
C 16	14.4	80.0	601	4	US-09-949-016-60604
C 17	14.4	80.0	601	4	US-09-949-016-60605
C 18	14.4	80.0	601	4	US-09-949-016-60606
C 19	14.4	80.0	1093	3	US-09-186-276B-53
C 20	14.4	80.0	1093	3	US-08-842-445-53
C 21	14.4	80.0	1093	3	US-09-186-188B-53
C 22	14.4	80.0	1093	3	US-09-265-585C-53
C 23	14.4	80.0	1629	4	US-09-919-039-32
C 24	14.4	80.0	1850	3	US-08-724-466B-3
C 25	14.4	80.0	1850	3	US-08-882-164D-3
C 26	14.4	80.0	1919	4	US-09-949-016-3746
C 27	14.4	80.0	3152	4	US-09-399-081A-7

C 28	14.4	80.0	6911	1	US-08-311-174-4
C 29	14.4	80.0	8878	1	US-08-206-176-3
C 30	14.4	80.0	12075	4	US-09-949-016-15488
C 31	14.4	80.0	91665	4	US-09-949-016-12234
C 32	14.4	80.0	283538	4	US-09-949-016-13506
C 33	14	77.8	1335	4	US-09-614-221A-167
C 34	14	77.8	22206	4	US-09-949-016-13901
C 35	14	77.8	58879	4	US-09-949-016-16052
C 36	14	77.8	177797	4	US-09-949-016-14125
C 37	14	77.8	227979	4	US-09-949-016-11842
C 38	14	77.8	246444	4	US-09-949-016-13113
C 39	13.8	76.7	432	4	US-09-513-999C-3262
C 40	13.8	76.7	514	4	US-09-389-681-417
C 41	13.8	76.7	514	4	US-09-620-405B-417
C 42	13.8	76.7	514	4	US-09-433-826B-417
C 43	13.8	76.7	514	4	US-09-604-287A-417
C 44	13.8	76.7	514	4	US-09-834-759-417
C 45	13.8	76.7	514	4	US-09-590-751A-417

ALIGNMENTS

RESULT 1
US-09-414-436-2/c
; Sequence 2, Application US/09414436
; Patent No. 6294384
; GENERAL INFORMATION:
; APPLICANT: Dell'Acqua, Giorgio
; APPLICANT: Mann, Michael J.
; TITLE OF INVENTION: Compositions and Methods Based Upon an Isoform of p53
; FILE REFERENCE: p53f
; CURRENT APPLICATION NUMBER: US/09/414,436
; CURRENT FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: 60/103,849
; EARLIER FILING DATE: 1999-10-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-09-414-436-2

Query Match 100.0%; Score 18; DB 3; Length 1415;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGACTGTGAATCTCCAT 18
Db 41 CGACTGTGAATCTCCAT 24
RESULT 2
US-08-184-009-214/c
; Sequence 214, Application US/08184009
; Patent No. 5833975
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I.
; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 217
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,009
; FILING DATE: 19-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2530
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066CURTMS
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1173 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-184-009-214

Query Match          91.1%; Score 16.4; DB 2; Length 1173;
Best Local Similarity 94.4%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGACTGTGAATCCTCCAT 18
        |||||
Db      27 CGACTGTGACTCTCCAT 10

RESULT 3
US-08-458-356-214/c
; Sequence 214, Application US/08458356
; Patent No. 5942235
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I.
; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 217
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,356
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/184,009
; FILING DATE: 19-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2530
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066CURTMS
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1173 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-458-356-214

Query Match          91.1%; Score 16.4; DB 2; Length 1173;
Best Local Similarity 94.4%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGACTGTGAATCCTCCAT 18
        |||||
Db      27 CGACTGTGACTCTCCAT 10

RESULT 4
US-08-796-101-45/c
; Sequence 45, Application US/08796101
; Patent No. 6183752
; GENERAL INFORMATION:
; APPLICANT: EPSTEIN, STEPHEN E.
; APPLICANT: FINKEL, TOREN
; APPLICANT: SPEIR, EDITH
; APPLICANT: ZHOU, YI FU
; APPLICANT: ZHU, JIANHUI
; APPLICANT: ERDILE, LORNE
; APPLICANT: PINCUS, STEVEN
; TITLE OF INVENTION: RESTENOSIS/ATHEROSCLEROSIS DIAGNOSIS,
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,101
; FILING DATE: 05-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: KOWALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 764-5574
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1173 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-796-101-45

Query Match          91.1%; Score 16.4; DB 3; Length 1173;
Best Local Similarity 94.4%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGACTGTGAATCCTCCAT 18
        |||||
Db      27 CGACTGTGACTCTCCAT 10

RESULT 5
US-08-460-736-214/c
; Sequence 214, Application US/08460736
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Patent No. 6265189
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,736
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 1173 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-08-460-736-214
Query Match 91.1%; Score 16.4; DB 3; Length 1173;
Best Local Similarity 94.4%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGACTGTGATCTCCAT 18
Db 27 CGACTGTGACTCTCCAT 10
RESULT 6
US-09-535-370-214/c
Sequence 214, Application US/09535370
Patent No. 6537594
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
Tartaglia, James
Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/535,370
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460,736
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 1173 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-535-370-214
Query Match 91.1%; Score 16.4; DB 4; Length 1173;
Best Local Similarity 94.4%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGACTGTGATCTCCAT 18
Db 27 CGACTGTGACTCTCCAT 10
RESULT 7
US-09-663-667-214/c
Sequence 214, Application US/09663667
Patent No. 6780407
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
Tartaglia, James
Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/663,667
FILING DATE: 15-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/184,009
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ ID NO: 214:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1173 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-663-667-214

Query Match          91.1%; Score 16.4; DB 4; Length 1173;
Best Local Similarity 94.4%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGACTGTGAATCCTCCAT 18
        |||||
DB      27 CGACTGTGAATCCTCCAT 10

RESULT 8
US-08-585-593A-36/c
; Sequence 36, Application US/08585593A
; Patent No. 6503706
; GENERAL INFORMATION:
; APPLICANT: ABKEN, Hinrich J
; APPLICANT: ALBERT, Winfried
; APPLICANT: JUNGPER, Herbert
; TITLE OF INVENTION: METHOD OF IDENTIFYING HUMAN AND ANIMAL
; TITLE OF INVENTION: CELLS CAPABLE OF UNLIMITED PROLIFERATION OR TUMOR
; TITLE OF INVENTION: FORMATION
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,593A
; FILING DATE: 16-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02307
; FILING DATE: 13-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 23 727.4
; FILING DATE: 15-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-585-593A-36

Query Match          85.6%; Score 15.4; DB 4; Length 396;
Best Local Similarity 94.1%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GACTGTGAATCCTCCAT 18
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DB      302 GACTCTGAATCCTCCAT 286

RESULT 9
US-09-621-976-1600
; Sequence 1600, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1600
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 136..435
; NAME/KEY: sig.peptide
; LOCATION: 136..279
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.8000019073486
; OTHER INFORMATION: seq ALLWAQEVGQVLA/GR
US-09-621-976-1600

Query Match          85.6%; Score 15.4; DB 4; Length 527;
Best Local Similarity 94.1%; Pred. No. 92;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGACTGTGAATCCTCCA 17
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DB      430 CGACTGTGAATCCTCCA 446

RESULT 10
US-09-270-767-14686/c
; Sequence 14686, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14686
; LENGTH: 2516
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-14686

Query Match          85.6%; Score 15.4; DB 4; Length 2516;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGACTGTGAATCCTCCA 17
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DB      811 CGACTGTGAATCCTCCA 795

RESULT 11
US-09-949-016-13319
; Sequence 13319, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
```

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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13319
; LENGTH: 103750
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13319

Query Match      85.6%; Score 15.4; DB 4; Length 103750;
Best Local Similarity 94.1%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGACTGTGAATCCTCCA 17
Db      7372 CCACGTGTGAATCCTCCA 7388

RESULT 12
US-09-328-475C-5/c
; Sequence 5, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-5

Query Match      83.3%; Score 15; DB 4; Length 1024;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ACTGTGAATCCTCCAT 18
Db      574 ACTGTGAATCCTCCAT 559

RESULT 13
US-09-248-796A-8906/c
; Sequence 8906, Application US/09248796A
; Patent No. 674137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 8906
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-8906

Query Match      82.2%; Score 14.8; DB 4; Length 1107;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGACTGTGAATCCTCCAT 18
Db      283 CTACTGGGAATCCTCCAT 266

RESULT 14
US-09-621-976-18989/c
; Sequence 18989, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18989
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-18989

Query Match      80.0%; Score 14.4; DB 4; Length 478;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ACTGTGAATCCTCCAT 18
Db      115 ACTGTGTATCCTCCAT 100

RESULT 15
US-09-949-016-60603/c
; Sequence 60603, Application US/09949016
; Patent No. 6812333
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 60603
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60603

Query Match 80.0%; Score 14.4; DB 4; Length 601;
Best Local Similarity 93.8%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ACTGTGAATCCTCCAT 18
|||||||
Db 245 ACTGTGAATCCTCCAT 230

Search completed: September 30, 2005, 13:08:55
Job time : 96.7368 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 06:14:52 ; Search time 3236.21 Seconds
(without alignments)
38.404 Million cell updates/sec

Title: US-09-578-453-1
Perfect score: 18
Sequence: 1 CGACTGTGAATCTCCAT 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7442561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 14885122

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
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8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18	100.0	25	21	US-10-822-235-3
C 2	18	100.0	1627	9	US-09-917-800A-1491
C 3	18	100.0	1627	17	US-10-388-934-568
C 4	16.4	91.1	390	9	US-09-974-300-3673
C 5	16.4	91.1	724	20	US-10-425-115-32582
C 6	16.4	91.1	1173	14	US-10-038-010-5
C 7	16.4	91.1	1173	16	US-10-267-384-214

C 8	16.4	91.1	1173	20	US-10-746-558-1	Sequence 1, Appl
C 9	16.4	91.1	1208	17	US-10-392-113-32	Sequence 32, Appl
C 10	16.4	91.1	1782	21	US-10-926-543-15	Sequence 15, Appl
C 11	15.4	85.6	441	18	US-10-424-599-102369	Sequence 102369,
C 12	15.4	85.6	458	13	US-10-027-632-285372	Sequence 285372,
C 13	15.4	85.6	458	17	US-10-027-632-285372	Sequence 285372,
C 14	15.4	85.6	584	20	US-10-653-047-6563	Sequence 6563, Ap
C 15	15.4	85.6	604	20	US-10-425-115-57974	Sequence 57974, A
C 16	15.4	85.6	608	14	US-10-052-283-349	Sequence 349, App
C 17	15.4	85.6	616	20	US-10-425-115-180675	Sequence 180675,
C 18	15.4	85.6	853	20	US-10-425-115-180677	Sequence 180677,
C 19	15.4	85.6	881	20	US-10-425-115-178848	Sequence 178848,
C 20	15.4	85.6	1017	20	US-10-425-115-180678	Sequence 180678,
C 21	15.4	85.6	1487	21	US-10-495-148-88	Sequence 88, Appl
C 22	15.4	85.6	1510	9	US-09-731-872-8	Sequence 8, Appl
C 23	15.4	85.6	1510	10	US-09-876-997-8	Sequence 8, Appl
C 24	15.4	85.6	1510	21	US-10-643-836-8	Sequence 8, Appl
C 25	15.4	85.6	1523	9	US-09-731-872-47	Sequence 47, Appl
C 26	15.4	85.6	1523	10	US-09-876-997-47	Sequence 47, Appl
C 27	15.4	85.6	1523	21	US-10-643-836-47	Sequence 47, Appl
C 28	15.4	85.6	1535	9	US-09-935-390A-15	Sequence 15, Appl
C 29	15.4	85.6	1664	21	US-10-887-553A-862	Sequence 862, App
C 30	15.4	85.6	1664	22	US-10-712-892A-19	Sequence 19, Appl
C 31	15.4	85.6	1684	22	US-10-475-856A-14	Sequence 14, Appl
C 32	15.4	85.6	1755	9	US-09-745-763-188	Sequence 188, App
C 33	15.4	85.6	1892	9	US-09-925-298-221	Sequence 221, App
C 34	15.4	85.6	1892	14	US-10-102-806-221	Sequence 221, App
C 35	15.4	85.6	2148	24	US-11-097-143-26261	Sequence 26261, A
C 36	15.4	85.6	2243	24	US-11-097-143-20729	Sequence 20729, A
C 37	15.4	85.6	3703	24	US-11-097-143-301	Sequence 301, App
C 38	15.4	85.6	4532	24	US-11-097-143-26260	Sequence 26260, A
C 39	15.4	85.6	4532	24	US-11-097-143-20728	Sequence 20728, A
C 40	15.4	85.6	154504	19	US-10-322-696-67	Sequence 67, Appl
C 41	15.4	85.6	200000	19	US-10-672-764A-33	Sequence 33, Appl
C 42	15.4	85.6	495635	22	US-10-737-082-12	Sequence 12, Appl
C 43	15.4	85.6	495635	22	US-10-765-790-12	Sequence 12, Appl
C 44	15.4	85.6	705636	22	US-10-737-082-30	Sequence 30, Appl
C 45	15.4	85.6	705636	22	US-10-765-790-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-10-822-235-3
; Sequence 3, Application US/10822235
; Publication No. US20050013855A1
; GENERAL INFORMATION:
; APPLICANT: Susan Gould-Fogerite
; APPLICANT: Raphael Mannino
; APPLICANT: Patrick Ahl
; APPLICANT: Gaofeng Shang
; APPLICANT: Zi Wei Chen
; APPLICANT: Sara Krause
; TITLE OF INVENTION: COCHLEATE COMPOSITIONS DIRECTED AGAINST
; FILE REFERENCE: BSZ-049
; CURRENT APPLICATION NUMBER: US/10/822,235
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53 antisense sequence
US-10-822-235-3

Query Match 100.0%; Score 18; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACTGTGAATCCTCCAT 18
Db 8 CGACTGTGAATCCTCCAT 25

RESULT 2

US-09-917-800A-1491/c
; Sequence 1491, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1491
; LENGTH: 1627
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 X13058

US-09-917-800A-1491

Query Match 100.0%; Score 18; DB 9; Length 1627;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACTGTGAATCCTCCAT 18
Db 41 CGACTGTGAATCCTCCAT 24

RESULT 3

US-10-388-934-568/c
; Sequence 568, Application US/10388934
; Publication No. US20040005547A1
; GENERAL INFORMATION:
; APPLICANT: Boess, Franziska
; APPLICANT: Suter-Dick, Laura
; APPLICANT: Wolf, Detlef
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
; FILE REFERENCE: 21199
; CURRENT APPLICATION NUMBER: US/10/388,934
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 02005336.9
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 02015657.6
; PRIOR FILING DATE: 2002-07-17

; NUMBER OF SEQ ID NOS: 862
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 568
; LENGTH: 1627
; TYPE: DNA
; ORGANISM: Rattus norvegicus (No. US20040005547A1way rat)
US-10-388-934-568

Query Match 100.0%; Score 18; DB 17; Length 1627;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACTGTGAATCCTCCAT 18
Db 41 CGACTGTGAATCCTCCAT 24

RESULT 4

US-09-974-300-3673/c
; Sequence 3673, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085-500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3673
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-3673

Query Match 91.1%; Score 16.4; DB 9; Length 390;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGACTGTGAATCCTCCAT 18
Db 120 CGACTGTGAATCCTCCAT 103

RESULT 5

US-10-425-115-32582/c
; Sequence 32582, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 32582
; LENGTH: 724
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(724)
; OTHER INFORMATION: unsure at all n locations

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; FEATURE:
; OTHER INFORMATION: Clone ID: MMT4577_129729C.1
; US-10-425-115-32582

Query Match          91.1%; Score 16.4; DB 20; Length 724;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGACTGTGAATCCTCCAT 18
||| ||||| ||||| |||||
Db 176 CGACTGTGACTCCTCCAT 159

RESULT 6
US-10-038-010-5/c
; Sequence 5, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: mouse p53
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1) ..(1173)
; OTHER INFORMATION: mouse p53 : Tumour suppressor protein
; US-10-038-010-5

Query Match          91.1%; Score 16.4; DB 14; Length 1173;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGACTGTGAATCCTCCAT 18
||| ||||| ||||| |||||
Db 27 CGACTGTGACTCCTCCAT 10

RESULT 7
US-10-267-384-214/c
; Sequence 214, Application US/10267384
; Publication No. US20030198623A1
; GENERAL INFORMATION:
; APPLICANT: Paolletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I.
; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 217
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,384
; FILING DATE: 09-Oct-2002
; CLASSIFICATION: 435

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; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066CURTMS
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1173 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-10-267-384-214

Query Match          91.1%; Score 16.4; DB 16; Length 1173;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGACTGTGAATCCTCCAT 18
||| ||||| ||||| |||||
Db 27 CGACTGTGACTCCTCCAT 10

RESULT 8
US-10-746-558-1/c
; Sequence 1, Application US/10746558
; Publication No. US20040208850A1
; GENERAL INFORMATION:
; APPLICANT: Ellenborn, Joshua D.I.
; APPLICANT: Diamond, Don J.
; TITLE OF INVENTION: Modified vaccinia Ankara expressing p53 in cancer immunotherapy
; FILE REFERENCE: 54435.8005-US00
; CURRENT APPLICATION NUMBER: US/10/746,558
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: 06/436,268
; PRIOR FILING DATE: 2002-12-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-746-558-1

Query Match          91.1%; Score 16.4; DB 20; Length 1173;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGACTGTGAATCCTCCAT 18
||| ||||| ||||| |||||
Db 27 CGACTGTGACTCCTCCAT 10

RESULT 9
US-10-392-113-32/c
; Sequence 32, Application US/10392113
; Publication No. US20030224993A1
; GENERAL INFORMATION:
; APPLICANT: Land, Hartmut
; APPLICANT: Deleu, Laurent
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
; FILE REFERENCE: 21108.0005U3
; CURRENT APPLICATION NUMBER: US/10/392,113
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15

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; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-392-113-32

Query Match      91.1%; Score 16.4; DB 17; Length 1208;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGACTGTGAATCCTCCAT 18
        |||||
Db      52 CGACTGTGAATCCTCCAT 35

RESULT 10
US-10-926-543-15/c
; Sequence 15, Application US/10926543
; Publication No. US20050048589A1
; GENERAL INFORMATION:
; APPLICANT: Jendoubi, Moncef
; TITLE OF INVENTION: LUNG CANCER SPECIFIC GENE PRODUCTS: THEIR CODING SEQUENCE, THEIR
; TITLE OF INVENTION: ANTIBODIES AND THEIR USE IN DIAGNOSTIC, THERAPEUTIC AND DISEASE
; TITLE OF INVENTION: MANAGEMENT OF LUNG CANCER
; FILE REFERENCE: 705403.4004
; CURRENT APPLICATION NUMBER: US/10/926,543
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US 60/497,790
; PRIOR FILING DATE: 2003-08-25
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 1782
; TYPE: DNA
; ORGANISM: Homo sapiens
- US-10-926-543-15

Query Match      91.1%; Score 16.4; DB 21; Length 1782;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGACTGTGAATCCTCCAT 18
        |||||
Db      155 CGACTGTGAATCCTCCAT 138

RESULT 11
US-10-424-599-102369/c
; Sequence 102369, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 102369
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_63456C.1
US-10-424-599-102369

Query Match      85.6%; Score 15.4; DB 18; Length 441;
Best Local Similarity 94.1%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GACTGTGAATCCTCCAT 18
        |||||
Db      236 GAATGTGAATCCTCCAT 220

RESULT 12
US-10-027-632-285372
; Sequence 285372, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 285372
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-285372

Query Match      85.6%; Score 15.4; DB 13; Length 458;
Best Local Similarity 94.1%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GACTGTGAATCCTCCAT 18
        |||||
Db      235 GACTGTGAATCCTCCAT 251

RESULT 13
US-10-027-632-285372
; Sequence 285372, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
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; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 285372
 ; LENGTH: 458
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-10-027-632-285372

Query Match 85.6%; Score 15.4; DB 17; Length 458;
 Best Local Similarity 94.1%; Pred. No. 4.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GACTGTGAATCCTCCAT 18
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 Db 235 GACTGTGAATCCTCCAT 251

RESULT 14

US-10-653-047-6563
 ; Sequence 6563, Application US/10653047
 ; Publication No. US20040229367A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Randy M. Berka
 ; APPLICANT: Michael W. Rey
 ; APPLICANT: Jeffrey R. Shuster
 ; APPLICANT: Sakari Kauppinen
 ; APPLICANT: Ib Groth Clausen
 ; APPLICANT: Peter Bjørke Olsen
 ; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
 ; FILE REFERENCE: 5849.200-US
 ; CURRENT APPLICATION NUMBER: US/10/653,047
 ; CURRENT FILING DATE: 2003-08-29
 ; PRIOR APPLICATION NUMBER: US/09/533,559
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 09/273,623
 ; PRIOR FILING DATE: 1999-03-22
 ; NUMBER OF SEQ ID NOS: 7860
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6563
 ; LENGTH: 584
 ; TYPE: DNA
 ; ORGANISM: Aspergillus oryzae
 ; US-10-653-047-6563

Query Match 85.6%; Score 15.4; DB 20; Length 584;
 Best Local Similarity 94.1%; Pred. No. 4.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GACTGTGAATCCTCCAT 18
 |||||
 Db 240 GATTGTGAATCCTCCAT 256

RESULT 15

US-10-425-115-57974
 ; Sequence 57974, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 57974
 ; LENGTH: 604
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(604)
 ; OTHER INFORMATION: unsure at all n locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_15286C.1
 ; US-10-425-115-57974

Query Match 85.6%; Score 15.4; DB 20; Length 604;
 Best Local Similarity 94.1%; Pred. No. 4.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGACTGTGAATCCTCCA 17
 |||||
 Db 420 CGACTGTGAATCCTCCA 436

Search completed: September 30, 2005, 15:13:54
 Job time : 3237.21 secs

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OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 06:14:52 ; Search time 3595.79 Seconds
(without alignments)
38.404 Million cell updates/sec

Title: US-09-578-453-2

Perfect score: 20

Sequence: 1 GGACATGCCCGCATGTCC 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7442561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 14885122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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- 10: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09D_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	17	US-10-447-136-162
2	20	100.0	20	17	US-10-447-136-162
3	20	100.0	24	14	US-10-023-318-19
4	20	100.0	24	14	US-10-023-318-19
5	20	100.0	24	14	US-10-023-318-38
6	20	100.0	24	14	US-10-023-318-38
7	19	95.0	19	16	US-10-339-161-14

RESULT 1

US-10-447-136-162
; Sequence 162, Application US/10447136
; Publication No. US20040009948A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and R2 Components of Ribonucleotide Reductase
; TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
; FILE REFERENCE: 032396-023
; CURRENT APPLICATION NUMBER: US/10/447,136
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/249,247
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/023,040
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/039,959
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/904,901
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-10-447-136-162

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1;

ALIGNMENTS

Sequence 14, Appl
Sequence 2482, Ap
Sequence 2482, Ap
Sequence 30682, A
Sequence 30682, A
Sequence 4271, Ap
Sequence 4271, Ap
Sequence 2765, Ap
Sequence 2765, Ap
Sequence 4270, Ap
Sequence 4270, Ap
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 61, Appl
Sequence 61, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 187, App
Sequence 187, App
Sequence 31, Appl
Sequence 31, Appl
Sequence 709, App
Sequence 709, App
Sequence 33, Appl
Sequence 33, Appl
Sequence 77, Appl
Sequence 77, Appl
Sequence 111, App
Sequence 111, App
Sequence 40, Appl
Sequence 40, Appl
Sequence 988, App
Sequence 988, App
Sequence 9, Appl
Sequence 9, Appl
Sequence 146659,
Sequence 146659,

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGGCATGTCC 20
|
Db 1 GGACATGCCCGGGCATGTCC 20

RESULT 2

US-10-447-136-162/c
; Sequence 162, Application US/10447136
; Publication No. US20040009948A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Alping H.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
; TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
; FILE REFERENCE: 032396-023
; CURRENT APPLICATION NUMBER: US/10/447,136
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/249,247
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/023,040
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/039,959
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/904,901
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-10-447-136-162

Query Match 100.0%; Score 20; DB 17; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

- Qy 1 GGACATGCCCGGGCATGTCC 20
|
Db 20 GGACATGCCCGGGCATGTCC 1

RESULT 3

US-10-023-318-19
; Sequence 19, Application US/10023318
; Publication No. US20030092015A1
; GENERAL INFORMATION:
; APPLICANT: Larose, Anne-Marie
; APPLICANT: Rousseau, Pierre
; APPLICANT: Leblanc, Benoit
; APPLICANT: Camato, Rino
; TITLE OF INVENTION: Method for Screening and/or Identifying Factors that
; TITLE OF INVENTION: Bind to Nucleic Acids
; FILE REFERENCE: 9555.123USU1
; CURRENT APPLICATION NUMBER: US/10/023,318
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 2,327,561
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NABE-probes
US-10-023-318-19

Query Match 100.0%; Score 20; DB 14; Length 24;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGGCATGTCC 20
|
Db 5 GGACATGCCCGGGCATGTCC 24

RESULT 4

US-10-023-318-19/c
; Sequence 19, Application US/10023318
; Publication No. US20030092015A1
; GENERAL INFORMATION:
; APPLICANT: Larose, Anne-Marie
; APPLICANT: Rousseau, Pierre
; APPLICANT: Leblanc, Benoit
; APPLICANT: Camato, Rino
; TITLE OF INVENTION: Method for Screening and/or Identifying Factors that
; TITLE OF INVENTION: Bind to Nucleic Acids
; FILE REFERENCE: 9555.123USU1
; CURRENT APPLICATION NUMBER: US/10/023,318
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 2,327,561
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NABE-probes
US-10-023-318-19

Query Match 100.0%; Score 20; DB 14; Length 24;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGGCATGTCC 20
|
Db 24 GGACATGCCCGGGCATGTCC 5

RESULT 5

US-10-023-318-38
; Sequence 38, Application US/10023318
; Publication No. US20030092015A1
; GENERAL INFORMATION:
; APPLICANT: Larose, Anne-Marie
; APPLICANT: Rousseau, Pierre
; APPLICANT: Leblanc, Benoit
; APPLICANT: Camato, Rino
; TITLE OF INVENTION: Method for Screening and/or Identifying Factors that
; TITLE OF INVENTION: Bind to Nucleic Acids
; FILE REFERENCE: 9555.123USU1
; CURRENT APPLICATION NUMBER: US/10/023,318
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 2,327,561
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Double
; OTHER INFORMATION: stranded NABE
US-10-023-318-38

Query Match 100.0%; Score 20; DB 14; Length 24;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGGCATGTCC 20

Db 5 GGACATGCCCGGCATGTC 24
|||||

RESULT 6
US-10-023-318-38/c
; Sequence 38, Application US/10023318
; Publication No. US20030092015A1
; GENERAL INFORMATION:
; APPLICANT: Larose, Anne-Marie
; APPLICANT: Rousseau, Pierre
; APPLICANT: Leblanc, Benoit
; APPLICANT: Camato, Rino
; TITLE OF INVENTION: Method for Screening and/or Identifying Factors that
; FILE REFERENCE: 9555.123USU1
; CURRENT APPLICATION NUMBER: US/10/023.318
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 2,327,561
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Double
; OTHER INFORMATION: stranded NABE
- US-10-023-318-38

Query Match 100.0%; Score 20; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGCATGTC 20
|||||

RESULT 7
US-10-339-161-14
; Sequence 14, Application US/10339161
; Publication No. US20030162211A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE DETERMINATION OF
; FILE REFERENCE: VANM212.001CP1
; CURRENT APPLICATION NUMBER: US/10/339.161
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor p53
US-10-339-161-14

Query Match 95.0%; Score 19; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGCATGTC 19
|||||

Db 1 GGACATGCCCGGCATGTC 19

RESULT 8
US-10-339-161-14/c
; Sequence 14, Application US/10339161
; Publication No. US20030162211A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE DETERMINATION OF
; FILE REFERENCE: VANM212.001CP1
; CURRENT APPLICATION NUMBER: US/10/339.161
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor p53
US-10-339-161-14

Query Match 95.0%; Score 19; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GACATGCCCGGCATGTC 20
|||||

RESULT 9
US-10-767-701-2482
; Sequence 2482, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 2482
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS41949_1
US-10-767-701-2482

Query Match 87.0%; Score 17.4; DB 19; Length 729;
Best Local Similarity 94.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGCATGTC 19
|||||

Db 247 GGACATGCCCGGCATGTC 265
|||||

RESULT 10
US-10-767-701-2482/c
; Sequence 2482, Application US/10767701

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; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 2482
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS41949_1
US-10-767-701-2482

Query Match      87.0%; Score 17.4; DB 19; Length 729;
Best Local Similarity 94.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GACATGCCCGGGCATGTCC 20
Db      265 GACATGCCCGGGCGGTGTC 247
      |||||
RESULT 11
US-10-425-114-30682
; Sequence 30682, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 30682
; LENGTH: 3325
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73063H08_FLI
US-10-425-114-30682

Query Match      87.0%; Score 17.4; DB 18; Length 3325;
Best Local Similarity 94.7%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGACATGCCCGGGCATGTC 19
Db      739 GGACACGCCCGGGCATGTC 757
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RESULT 12
US-10-425-114-30682/c
; Sequence 30682, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 30682
; LENGTH: 3325
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73063H08_FLI
US-10-425-114-30682

Query Match      87.0%; Score 17.4; DB 18; Length 3325;
Best Local Similarity 94.7%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGACATGCCCGGGCATGTC 19
Db      739 GGACACGCCCGGGCATGTC 757
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RESULT 13
US-10-425-115-4271
; Sequence 4271, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 4271
; LENGTH: 3458
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_103895C.1
US-10-425-115-4271

Query Match      87.0%; Score 17.4; DB 20; Length 3458;
Best Local Similarity 94.7%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGACATGCCCGGGCATGTC 19
Db      739 GGACACGCCCGGGCATGTC 757
      |||||
RESULT 14
US-10-425-115-4271/c
; Sequence 4271, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 4271
; LENGTH: 3458
; TYPE: DNA
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; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_103895C.1
US-10-425-115-4271

Query Match      87.0%; Score 17.4; DB 20; Length 3458;
Best Local Similarity 94.7%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GACATGCCCGGGCATGTCC 20
      |||||
Db      757 GACATGCCCGGGCATGTCC 739

RESULT 15
US-10-425-114-2765
; Sequence 2765, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2765
; LENGTH: 3569
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700223564_FLI
US-10-425-114-2765

Query Match      87.0%; Score 17.4; DB 18; Length 3569;
Best Local Similarity 94.7%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGACATGCCCGGGCATGTC 19
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Db      733 GGACATGCCCGGGCATGTC 751

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OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 05:40:32 ; Search time 105.263 Seconds
(without alignments)
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Title: US-09-578-453-2
Perfect score: 20
Sequence: 1 GGACATGCCCGGCATGTCC 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	US-08-904-901-162
2	20	100.0	20	2	US-08-904-901-162
3	20	100.0	20	3	US-09-249-730-162
4	20	100.0	20	3	US-09-249-730-162
5	20	100.0	20	4	US-09-249-247-162
6	20	100.0	20	4	US-09-249-247-162
7	20	100.0	26	3	US-08-767-942A-40
8	20	100.0	26	3	US-08-767-942A-40
9	20	100.0	27	3	US-08-767-942A-41
10	20	100.0	27	3	US-08-767-942A-41
11	16.8	84.0	30	1	US-08-347-792-18
12	16.8	84.0	30	1	US-08-347-792-18
13	16.8	84.0	30	1	US-08-431-357-18
14	16.8	84.0	30	1	US-08-431-357-18
15	16.8	84.0	30	2	US-08-697-221-29
16	16.8	84.0	30	2	US-08-697-221-29
17	16.8	84.0	30	3	US-08-392-542-31
18	16.8	84.0	30	3	US-08-392-542-31
19	16.8	84.0	30	3	US-08-894-327-31
20	16.8	84.0	30	3	US-08-894-327-31
21	16.8	84.0	30	3	US-09-685-027-31
22	16.8	84.0	30	3	US-09-685-027-31
23	16.8	84.0	30	4	US-09-829-922-31
24	16.8	84.0	30	4	US-09-829-922-31
25	16.8	84.0	30	5	PCT-US95-15353-18
26	16.8	84.0	30	5	PCT-US95-15353-18
27	16.8	84.0	9391	4	US-09-562-702A-11

c 28	16.8	84.0	9391	4	US-09-562-702A-11	Sequence 11, Appl
29	16.8	84.0	9511	4	US-09-562-702A-9	Sequence 9, Appl1
c 30	16.8	84.0	9511	4	US-09-562-702A-9	Sequence 9, Appl1
c 31	15.8	79.0	41927	4	US-09-902-540-1268	Sequence 1268, Ap
c 32	15.8	79.0	41927	4	US-09-902-540-1268	Sequence 1268, Ap
c 33	15.4	77.0	473	4	US-09-312-283C-355	Sequence 355, App
c 34	15.4	77.0	473	4	US-09-312-283C-355	Sequence 355, App
c 35	15.4	77.0	601	4	US-09-949-016-136475	Sequence 136475,
c 36	15.4	77.0	601	4	US-09-949-016-136475	Sequence 136475,
c 37	15.4	77.0	97423	4	US-09-949-016-12742	Sequence 12742, A
c 38	15.4	77.0	97423	4	US-09-949-016-12742	Sequence 12742, A
c 39	15.4	77.0	97424	4	US-09-949-016-15576	Sequence 15576, A
c 40	15.4	77.0	97424	4	US-09-949-016-15576	Sequence 15576, A
c 41	15.2	76.0	20	2	US-08-657-828A-3	Sequence 3, Appl1
c 42	15.2	76.0	20	2	US-08-657-828A-3	Sequence 3, Appl1
c 43	15.2	76.0	20	3	US-09-260-420-3	Sequence 3, Appl1
c 44	15.2	76.0	20	3	US-09-260-420-3	Sequence 3, Appl1
c 45	15.2	76.0	291	4	US-09-513-999C-22333	Sequence 22333, A

ALIGNMENTS

RESULT 1
US-08-904-901-162
; Sequence 162, Application US/08904901
; Patent No. 5998383
; GENERAL INFORMATION:
; APPLICANT: Wright, Jim A.
; APPLICANT: Young, Aiping H.
; TITLE OF INVENTION: ANTITUMOR ANTISENSE SEQUENCES DIRECTED
; AGAINST RIBONUCLEOTIDE REDUCTASE
; NUMBER OF SEQUENCES: 163
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 5998383thwestern Hwy. Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,901
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 0227.00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Primer"
US-08-904-901-162

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGACATGCCCGGCATGTCC 20
Db 1 GGACATGCCCGGCATGTCC 20

RESULT 2
US-08-904-901-162/c
; Sequence 162, Application US/08904901
; Patent No. 599383
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: ANTITUMOR ANTISENSE SEQUENCES DIRECTED
; TITLE OF INVENTION: AGAINST RIBONUCLEOTIDE REDUCTASE
; NUMBER OF SEQUENCES: 163
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 NO. 5998383thwestern Hwy. Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: 163
; APPLICATION NUMBER: US/08/904,901
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 0227.00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Primer"
US-08-904-901-162

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGGCATGTCC 20
Db 20 GGACATGCCCGGGCATGTCC 1

RESULT 3
US-09-249-730-162
; Sequence 162, Application US/09249730
; Patent No. 6121000
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
; TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
; FILE REFERENCE: 032396-040
; CURRENT APPLICATION NUMBER: US/09/249,730
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-249-730-162

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGGCATGTCC 20
Db 1 GGACATGCCCGGGCATGTCC 20

RESULT 4
US-09-249-730-162/c
; Sequence 162, Application US/09249730
; Patent No. 6121000
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
; TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
; FILE REFERENCE: 032396-040
; CURRENT APPLICATION NUMBER: US/09/249,730
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-249-730-162

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGGCATGTCC 20
Db 20 GGACATGCCCGGGCATGTCC 1

RESULT 5
US-09-249-247-162
; Sequence 162, Application US/09249247
; Patent No. 6593305
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
; TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
; FILE REFERENCE: 032396-023
; CURRENT APPLICATION NUMBER: US/09/249,247
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: US 60/023,040
; EARLIER FILING DATE: 1996-08-02
; EARLIER APPLICATION NUMBER: US 60/039,959
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: US 08/904,901
; EARLIER FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-249-247-162

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGGCATGTCC 20
Db 1 GGACATGCCCGGGCATGTCC 20

RESULT 6
US-09-249-247-162/c
; Sequence 162, Application US/09249247
; Patent No. 6593305
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
; TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
; FILE REFERENCE: 032396-023
; CURRENT APPLICATION NUMBER: US/09/249,247
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: US 60/023,040
; EARLIER FILING DATE: 1996-08-02
; EARLIER APPLICATION NUMBER: US 60/039,959
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: US 08/904,901
; EARLIER FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
~ US-09-249-247-162

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GGACATGCCCGGCATGTCC 20
Db 20 GGACATGCCCGGCATGTCC 1

RESULT 7
US-08-767-942A-40
; Sequence 40, Application US/08767942A
; Patent No. 6068982
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Chiu, M. Isabel
; APPLICANT: Berlin, Vivian
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume, Cottarel
; TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-767-942A-40

Query Match 100.0%; Score 20; DB 3; Length 26;

Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGCATGTCC 20
Db 25 GGACATGCCCGGCATGTCC 6

RESULT 9
US-08-767-942A-41
; Sequence 41, Application US/08767942A
; Patent No. 6068982

; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-767-942A-40

Query Match 100.0%; Score 20; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGCATGTCC 20
Db 6 GGACATGCCCGGCATGTCC 25

RESULT 8
US-08-767-942A-40/c
; Sequence 40, Application US/08767942A
; Patent No. 6068982
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Chiu, M. Isabel
; APPLICANT: Berlin, Vivian
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume, Cottarel
; TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-767-942A-40

Query Match 100.0%; Score 20; DB 3; Length 26;

Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGCATGTCC 20
Db 25 GGACATGCCCGGCATGTCC 6

;
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Chiu, M. Isabel
; APPLICANT: Berlin, Vivian
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume, Cottarel
; TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-767-942A-41

Query Match 100.0%; Score 20; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATCCCGGGCATGTCC 20
Db 7 GGACATCCCGGGCATGTCC 26

RESULT 10
US-08-767-942A-41/c
; Sequence 41, Application US/08767942A
; Patent No. 6068982
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Chiu, M. Isabel
; APPLICANT: Berlin, Vivian
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume, Cottarel
; TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-767-942A-41

Query Match 100.0%; Score 20; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATCCCGGGCATGTCC 20
Db 26 GGACATCCCGGGCATGTCC 7

RESULT 11
US-08-347-792-18
; Sequence 18, Application US/08347792
; Patent No. 5573925
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos D.
; TITLE OF INVENTION: p53 Proteins With Altered
; STRANDEDNESS: Tetramerization Domains
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,792
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST58USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-347-792-18

Query Match 84.0%; Score 16.8; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGCATGTCC 20
|||
Db 3 GGGCATGTCCGGGCATGTCC 22

RESULT 12

US-08-347-792-18/c
; Sequence 18, Application US/08347792
; Patent No. 5573925
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos D.
; TITLE OF INVENTION: p53 Proteins With Altered
; TITLE OF INVENTION: Tetramerization Domains
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,792
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST58USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-347-792-18

Query Match 84.0%; Score 16.8; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGCATGTCC 20
|||
Db 22 GGACATGCCCGGCATGTCC 3

RESULT 13

US-08-431-357-18
; Sequence 18, Application US/08431357
; Patent No. 5721340
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos D.
; TITLE OF INVENTION: p53 Proteins With Altered
; TITLE OF INVENTION: Tetramerization Domains
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,357
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/347,792
; FILING DATE: 28-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST58USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-431-357-18

Query Match 84.0%; Score 16.8; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGCATGTCC 20
|||
Db 3 GGGCATGTCCGGGCATGTCC 22

RESULT 14

US-08-431-357-18/c
; Sequence 18, Application US/08431357
; Patent No. 5721340
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos D.
; TITLE OF INVENTION: p53 Proteins With Altered
; TITLE OF INVENTION: Tetramerization Domains
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,357
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/347,792
; FILING DATE: 28-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST58USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:

;
;
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-431-357-18

Query Match 84.0%; Score 16.8; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGCATGTCC 20
|||
Db 22 GGACATGCCCGGCATGTCCC 3

RESULT 15
US-08-697-221-29
; Sequence 29, Application US/08697221
; Patent No. 5847083
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos D.
; TITLE OF INVENTION: Modified p53 Constructs and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/697,221
; FILING DATE:
; APPLICATION NUMBER: US/08/697,221
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,802
; FILING DATE: 22-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST64AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-697-221-29

Query Match 84.0%; Score 16.8; DB 2; Length 30;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGACATGCCCGGCATGTCC 20
|||
Db 3 GGACATGCCCGGCATGTCCC 22

Search completed: September 30, 2005, 13:08:56
Job time : 106.263 secs